

SCORE Search Results Details for Application 10626891 and Search Result us-10-626-891-1_copy_1_332.rge.

[Score](#) [Home](#)
[Page](#)

Retrieve Application List

SCORE System Overview

SCORE
FAQ

Comments /
Suggestions

This page gives you Search Results detail for the Application 10626891 and Search Result us-10-626-891-1_copy_1_332.rge.

start

[Go Back to previous page](#)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

```
Run on:      June  1, 2006, 13:09:12 ; Search time 2987.25 Seconds
              (without alignments)
              7107.048 Million cell updates/sec
```

```
Title:          US-10-626-891-1_COPY_1_332
Perfect score:  332
Sequence:       1 ccagaaggttaattatccaag.....atgtaagggcggaagtaac.332
```

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	332	100.0	515	2	BD262203	BD262203 Chimeric
2	332	100.0	515	2	AR439662	AR439662 Sequence
3	332	100.0	515	2	AR765039	AR765039 Sequence
4	332	100.0	515	2	AX036736	AX036736 Sequence
5	332	100.0	515	2	AX088388	AX088388 Sequence
6	332	100.0	532	2	AX202413	AX202413 Sequence
7	332	100.0	538	2	CQ828123	CQ828123 Sequence
8	332	100.0	538	2	CQ828192	CQ828192 Sequence
9	332	100.0	538	2	CQ830297	CQ830297 Sequence
10	332	100.0	593	2	AR439664	AR439664 Sequence
11	332	100.0	593	2	AX088390	AX088390 Sequence
12	332	100.0	710	2	CQ828124	CQ828124 Sequence
13	332	100.0	710	2	CQ828193	CQ828193 Sequence
14	332	100.0	838	2	BD205013	BD205013 Gene enco
15	332	100.0	838	2	AR697948	AR697948 Sequence
16	332	100.0	838	2	AX014764	AX014764 Sequence
17	332	100.0	853	2	AR439663	AR439663 Sequence
18	332	100.0	853	2	AX088389	AX088389 Sequence
19	332	100.0	857	2	AR439665	AR439665 Sequence
20	332	100.0	857	2	AX088391	AX088391 Sequence
21	332	100.0	931	2	AR439666	AR439666 Sequence
22	332	100.0	931	2	AR439667	AR439667 Sequence
c 23	332	100.0	931	2	AR439667	AR439667 Sequence
24	332	100.0	931	2	AX088392	AX088392 Sequence
25	332	100.0	931	2	AX088393	AX088393 Sequence
c 26	332	100.0	931	2	AX088393	AX088393 Sequence
27	332	100.0	1036	2	BD205014	BD205014 Gene enco
28	332	100.0	1036	2	AR697949	AR697949 Sequence
29	332	100.0	1036	2	AX014765	AX014765 Sequence
30	332	100.0	8158	10	CVU20341	U20341 Cassava vei
31	332	100.0	8159	10	CVU59751	U59751 Cassava vei
c 32	331	99.7	8340	2	AR275735	AR275735 Sequence
c 33	331	99.7	8340	2	AR321647	AR321647 Sequence
c 34	331	99.7	8340	2	AX329231	AX329231 Sequence
c 35	331	99.7	8340	2	AX338536	AX338536 Sequence
c 36	330.4	99.5	12241	2	AX412168	AX412168 Sequence
37	219	66.0	219	2	CQ828120	CQ828120 Sequence
38	219	66.0	219	2	CQ828189	CQ828189 Sequence
39	115.4	34.8	317	2	BD262204	BD262204 Chimeric
40	115.4	34.8	317	2	AR765040	AR765040 Sequence
41	115.4	34.8	317	2	AX036737	AX036737 Sequence
42	115.4	34.8	371	2	BD262206	BD262206 Chimeric
43	115.4	34.8	371	2	AR765042	AR765042 Sequence
44	115.4	34.8	371	2	AX036739	AX036739 Sequence
45	115.4	34.8	392	2	BD262222	BD262222 Chimeric

ALIGNMENTS

RESULT 1
BD262203

SCORE Search Results Details for Application 10626891 and Search Result us-10-626-891-1_copy_1_332.rng.

[Score Home](#)
[Page](#)

Retrieve Application List

SCORE System Overview

SCORE
FAQ

Comments /
Suggestions

This page gives you Search Results detail for the Application 10626891 and Search Result us-10-626-891-1_copy_1_332.rng.

start

[Go Back to previous page](#)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

```
Run on:      June  1, 2006, 12:57:52 ; Search time 489.027 Seconds
              (without alignments)
              4733.453 Million cell updates/sec
```

Title: US-10-626-891-1_COPY_1_332
Perfect score: 332
Sequence: 1 ccagaaggttaattatccaag.....atgtaagggcggaagtaac 332

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

```

```
Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	332	100.0	515	3	AAA96836	Aaa96836 Promoter
2	332	100.0	515	4	AAF55505	Aaf55505 Nucleotid
3	332	100.0	524	2	AAV14020	Aav14020 CsVMV pro
4	332	100.0	526	2	AAV14018	Aav14018 CsVMV pro
5	332	100.0	532	4	AAD11575	Aad11575 Cassava V
6	332	100.0	538	12	ADO85792	Ado85792 Promoter
7	332	100.0	538	12	ADO59549	Ado59549 pSF29 vec
8	332	100.0	538	12	ADO54812	Ado54812 Cassava v
9	332	100.0	593	4	AAF55507	Aaf55507 Nucleotid
10	332	100.0	710	12	ADO59550	Ado59550 Double Cs
11	332	100.0	710	12	ADO54813	Ado54813 Cassava v
12	332	100.0	853	4	AAF55506	Aaf55506 Nucleotid
13	332	100.0	857	4	AAF55508	Aaf55508 Nucleotid
14	332	100.0	931	4	AAF55509	Aaf55509 Nucleotid
15	332	100.0	931	4	AAF55510	Aaf55510 Nucleotid
c 16	332	100.0	931	4	AAF55510	Aaf55510 Nucleotid
17	332	100.0	1839	6	ABL57988	Abl57988 4-Hydroxy
18	332	100.0	4133	14	AEC80297	Aec80297 Plasmid p
19	332	100.0	4133	14	AEC80296	Aec80296 Plasmid p
20	332	100.0	4136	14	AEC80294	Aec80294 Plasmid p
21	332	100.0	4136	14	AEC80295	Aec80295 Plasmid p
22	332	100.0	4287	14	AEC80300	Aec80300 Plasmid p
23	332	100.0	4287	14	AEC80301	Aec80301 Plasmid p
24	332	100.0	4290	14	AEC80299	Aec80299 Plasmid p
25	332	100.0	4290	14	AEC80298	Aec80298 Plasmid p
26	332	100.0	4677	6	ABL57989	Abl57989 4-Hydroxy
27	332	100.0	4767	13	ADU69198	Adu69198 pCHN-18 m
28	332	100.0	8187	6	ABL58082	Abl58082 4-Hydroxy
c 29	332	100.0	10575	13	ADU69210	Adu69210 Vector pC
c 30	332	100.0	10603	13	ADU69212	Adu69212 Vector pC
c 31	332	100.0	10677	13	ADU69211	Adu69211 Vector pM
32	331	99.7	1052	6	ABS53107	Abs53107 Transgene
33	331	99.7	1590	6	ABS53109	Abs53109 Transgene
c 34	331	99.7	8340	6	AAD24139	Aad24139 pAGI4002
c 35	331	99.7	8340	6	ABA04755	Aba04755 Binary ve
c 36	330.4	99.5	12241	6	AAD36732	Aad36732 Binary ve
c 37	330.4	99.5	12241	6	ABQ73049	Abq73049 Tomato an
c 38	330.4	99.5	12241	11	ADO05418	Ado05418 Binary ve
39	328.8	99.0	476	2	AAV14053	Aav14053 CsVMV pro
40	317	95.5	552	15	AEF22368	Aef22368 Cassava v
41	297.6	89.6	441	2	AAV14033	Aav14033 CsVMV pro
42	296.2	89.2	491	2	AAV14030	Aav14030 CsVMV pro
c 43	278	83.7	1590	6	ABS53109	Abs53109 Transgene
44	271	81.6	418	2	AAV14032	Aav14032 CsVMV pro
45	271	81.6	468	2	AAV14029	Aav14029 CsVMV pro

ALIGNMENTS

RESULT 1
AAA96836

SCORE Search Results Details for Application 10626891 and Search Result us-10-626-891- 1_copy_1_332.rni.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Sugg](#)

This page gives you Search Results detail for the Application 10626891 and Search Result us-10-626-891-1_copy_1_332.rni.

[start](#)

[Go Back to pre](#)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 1, 2006, 14:04:52 ; Search time 129.36 Seconds
(without alignments)
4802.152 Million cell updates/sec

Title: US-10-626-891-1_COPY_1_332
Perfect score: 332
Sequence: 1 ccagaaggtattatccaag.....atgtaaggcgaaagtaac 332

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	332	100.0	515	3	US-09-641-466-1	Sequence 1, Appli
2	332	100.0	515	4	US-09-963-803-2	Sequence 2, Appli
3	332	100.0	593	3	US-09-641-466-3	Sequence 3, Appli
4	332	100.0	838	3	US-09-673-274C-19	Sequence 19, Appl
5	332	100.0	853	3	US-09-641-466-2	Sequence 2, Appli
6	332	100.0	857	3	US-09-641-466-4	Sequence 4, Appli
7	332	100.0	931	3	US-09-641-466-5	Sequence 5, Appli
8	332	100.0	931	3	US-09-641-466-6	Sequence 6, Appli
c 9	332	100.0	931	3	US-09-641-466-6	Sequence 6, Appli
10	332	100.0	1036	3	US-09-673-274C-20	Sequence 20, Appl
c 11	331	99.7	8340	3	US-09-847-057-4	Sequence 4, Appli
c 12	331	99.7	8340	3	US-09-874-926-4	Sequence 4, Appli
c 13	330.4	99.5	12241	3	US-09-948-138-4	Sequence 4, Appli
c 14	330.4	99.5	12241	5	US-10-033-190-5	Sequence 5, Appli
15	115.4	34.8	317	4	US-09-963-803-3	Sequence 3, Appli
16	115.4	34.8	371	4	US-09-963-803-5	Sequence 5, Appli
17	115.4	34.8	392	4	US-09-963-803-21	Sequence 21, Appl
18	115.4	34.8	393	4	US-09-963-803-19	Sequence 19, Appl
19	115.4	34.8	462	4	US-09-963-803-20	Sequence 20, Appl
20	115.4	34.8	600	4	US-09-963-803-22	Sequence 22, Appl
21	103.4	31.1	301	4	US-09-963-803-7	Sequence 7, Appli
22	103.4	31.1	348	4	US-09-963-803-4	Sequence 4, Appli
23	103.4	31.1	398	4	US-09-963-803-6	Sequence 6, Appli
24	103.4	31.1	472	4	US-09-963-803-25	Sequence 25, Appl
25	103.4	31.1	541	4	US-09-963-803-24	Sequence 24, Appl
26	103.4	31.1	604	4	US-09-963-803-23	Sequence 23, Appl
c 27	73.4	22.1	7218	2	US-08-232-463-14	Sequence 14, Appl
28	62	18.7	62	4	US-09-963-803-10	Sequence 10, Appl
29	47.2	14.2	1685	3	US-10-104-047-1957	Sequence 1957, Ap
30	45	13.6	113876	3	US-09-949-016-14828	Sequence 14828, A
31	45	13.6	113876	3	US-09-949-016-14829	Sequence 14829, A
32	45	13.6	115508	3	US-09-949-016-11800	Sequence 11800, A
33	45	13.6	115508	3	US-09-949-016-14826	Sequence 14826, A
34	45	13.6	115508	3	US-09-949-016-14827	Sequence 14827, A
35	44.6	13.4	3279	3	US-08-446-137B-1	Sequence 1, Appli
36	43.4	13.1	700	3	US-09-735-271-796	Sequence 796, App
37	43.4	13.1	700	3	US-09-735-271-797	Sequence 797, App
c 38	43.4	13.1	50000	5	US-09-396-985B-48	Sequence 48, Appl
c 39	43.4	13.1	64309	3	US-09-949-016-14581	Sequence 14581, A
c 40	43.4	13.1	89625	3	US-09-949-016-17012	Sequence 17012, A
c 41	43.2	13.0	929	3	US-09-671-317-14	Sequence 14, Appl
c 42	43.2	13.0	1001	3	US-09-671-317-439	Sequence 439, App
43	42.8	12.9	106746	3	US-09-326-402C-1	Sequence 1, Appli
44	42.8	12.9	106746	3	US-09-326-402C-12	Sequence 12, Appl
45	42.6	12.8	5433	3	US-08-929-329-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-641-466-1

; Sequence 1, Application US/09641466

; Patent No. 6664384

; GENERAL INFORMATION:

; APPLICANT: Xu, Dongmei

; APPLICANT: Nielsen, Mark T.

; TITLE OF INVENTION: Duplicated Cassava Vein Mosaic Virus

SCORE Search Results Details for Application 10626891 and Search Result us-10-626-891-1_copy_1_332.rnpbm.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Sugg](#)

This page gives you Search Results detail for the Application 10626891 and Search Result us-10-626-891-1_copy_1_332.rnpbm.

[start](#)

[Go Back to previc](#)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 1, 2006, 14:09:06 ; Search time 1882.08 Seconds
(without alignments)
2167.545 Million cell updates/sec

Title: US-10-626-891-1_COPY_1_332
Perfect score: 332
Sequence: 1 ccagaaggttaattatccaag.....atgtaaggcggaagtaac 332

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	332	100.0	515	3	US-09-963-803-2	Sequence 2, Appli
2	332	100.0	515	10	US-10-626-891-1	Sequence 1, Appli
3	332	100.0	524	16	US-11-191-658-2	Sequence 2, Appli
4	332	100.0	524	16	US-11-191-658-3	Sequence 3, Appli
5	332	100.0	532	3	US-09-765-555-1	Sequence 1, Appli
6	332	100.0	593	10	US-10-626-891-3	Sequence 3, Appli
7	332	100.0	853	10	US-10-626-891-2	Sequence 2, Appli
8	332	100.0	857	10	US-10-626-891-4	Sequence 4, Appli
9	332	100.0	931	10	US-10-626-891-5	Sequence 5, Appli
10	332	100.0	931	10	US-10-626-891-6	Sequence 6, Appli
c 11	332	100.0	931	10	US-10-626-891-6	Sequence 6, Appli
12	332	100.0	1839	8	US-10-415-302-19	Sequence 19, Appl
13	332	100.0	4133	15	US-11-069-601-7	Sequence 7, Appli
14	332	100.0	4133	15	US-11-069-601-8	Sequence 8, Appli
15	332	100.0	4136	15	US-11-069-601-5	Sequence 5, Appli
16	332	100.0	4136	15	US-11-069-601-6	Sequence 6, Appli
17	332	100.0	4287	15	US-11-069-601-11	Sequence 11, Appl
18	332	100.0	4287	15	US-11-069-601-12	Sequence 12, Appl
19	332	100.0	4290	15	US-11-069-601-9	Sequence 9, Appli
20	332	100.0	4290	15	US-11-069-601-10	Sequence 10, Appl
21	332	100.0	4677	8	US-10-415-302-21	Sequence 21, Appl
22	332	100.0	4767	9	US-10-838-834-12	Sequence 12, Appl
23	332	100.0	8187	8	US-10-415-302-22	Sequence 22, Appl
c 24	332	100.0	10575	9	US-10-838-834-24	Sequence 24, Appl
c 25	332	100.0	10603	9	US-10-838-834-26	Sequence 26, Appl
c 26	332	100.0	10677	9	US-10-838-834-25	Sequence 25, Appl
27	331	99.7	1052	10	US-10-075-105C-5	Sequence 5, Appli
28	331	99.7	1590	10	US-10-075-105C-7	Sequence 7, Appli
c 29	331	99.7	8340	3	US-09-847-057-4	Sequence 4, Appli
c 30	331	99.7	8340	3	US-09-874-926-4	Sequence 4, Appli
c 31	330.4	99.5	12241	3	US-09-948-138-4	Sequence 4, Appli
c 32	330.4	99.5	12241	6	US-10-033-190-5	Sequence 5, Appli
c 33	330.4	99.5	12241	7	US-10-407-845A-4	Sequence 4, Appli
c 34	330.4	99.5	12241	10	US-10-510-249-4	Sequence 4, Appli
35	328.8	99.0	476	16	US-11-191-658-17	Sequence 17, Appl
36	317	95.5	552	11	US-10-888-613B-67	Sequence 67, Appl
37	297.6	89.6	441	16	US-11-191-658-16	Sequence 16, Appl
38	296.2	89.2	491	16	US-11-191-658-13	Sequence 13, Appl
c 39	278	83.7	1590	10	US-10-075-105C-7	Sequence 7, Appli
40	271	81.6	418	16	US-11-191-658-15	Sequence 15, Appl
41	271	81.6	468	16	US-11-191-658-12	Sequence 12, Appl
42	261.4	78.7	408	16	US-11-191-658-14	Sequence 14, Appl
43	261.4	78.7	458	16	US-11-191-658-11	Sequence 11, Appl
44	259	78.0	392	16	US-11-191-658-1	Sequence 1, Appli
45	230.8	69.5	482	16	US-11-191-658-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-09-963-803-2

SCORE Search Results Details for Application 10626891 and Search Result us-10-626-891-1_copy_1_332.rnpbn.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10626891 and Search Result us-10-626-891-1_copy_1_332.rnpbn.

start

[Go Back to previous page](#)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

```
Run on:      June  1, 2006, 14:12:07 ; Search time 56.0811 Seconds
              (without alignments)
              697.222 Million cell updates/sec
```

```
Title:          US-10-626-891-1_COPY_1_332
Perfect score:  332
Sequence:       1 ccagaagqtaattatccaag.....atgtaagggcggaagtaac 332
```

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 246837 seqs, 58886990 residues

Total number of hits satisfying chosen parameters: 493674

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      Published_Applications_NA_New:*
1:  /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2:  /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3:  /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4:  /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5:  /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6:  /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7:  /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8:  /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
--------	------------

No.	Score	Match	Length	DB	ID	Description
1	47	14.2	633	7	US-11-217-529-2794	Sequence 2794, Ap
2	45	13.6	1828	6	US-10-953-349-4999	Sequence 4999, Ap
c 3	44	13.3	372	7	US-11-217-529-174580	Sequence 174580,
4	44	13.3	1908	7	US-11-217-529-82752	Sequence 82752, A
c 5	41.8	12.6	531	7	US-11-217-529-5508	Sequence 5508, Ap
6	41.6	12.5	534	7	US-11-217-529-82693	Sequence 82693, A
7	41.2	12.4	1426	6	US-10-953-349-11399	Sequence 11399, A
8	40.8	12.3	1785	7	US-11-217-529-2048	Sequence 2048, Ap
c 9	40.4	12.2	366	7	US-11-217-529-174036	Sequence 174036,
10	40.4	12.2	444	7	US-11-217-529-76472	Sequence 76472, A
11	40.4	12.2	3108	7	US-11-217-529-2842	Sequence 2842, Ap
12	39.8	12.0	3735	7	US-11-217-529-2189	Sequence 2189, Ap
c 13	39.4	11.9	282	7	US-11-217-529-174544	Sequence 174544,
14	39.4	11.9	1344	7	US-11-217-529-882	Sequence 882, App
c 15	38.8	11.7	1046	6	US-10-953-349-39955	Sequence 39955, A
16	38.8	11.7	2272	6	US-10-953-349-37381	Sequence 37381, A
17	38.4	11.6	852	7	US-11-217-529-79907	Sequence 79907, A
18	38.4	11.6	1269	7	US-11-217-529-75	Sequence 75, Appl
c 19	38.2	11.5	1731	7	US-11-217-529-79078	Sequence 79078, A
20	38.2	11.5	2209	6	US-10-953-349-23348	Sequence 23348, A
21	37.8	11.4	2139	7	US-11-217-529-2026	Sequence 2026, Ap
22	37.6	11.3	576	7	US-11-217-529-166604	Sequence 166604,
c 23	37.6	11.3	1712	6	US-10-953-349-10075	Sequence 10075, A
24	37.6	11.3	5373	7	US-11-217-529-5516	Sequence 5516, Ap
25	37.2	11.2	1803	7	US-11-217-529-79814	Sequence 79814, A
c 26	37	11.1	1176	7	US-11-217-529-81002	Sequence 81002, A
27	37	11.1	1818	7	US-11-217-529-3228	Sequence 3228, Ap
c 28	37	11.1	1859	7	US-11-293-697-2286	Sequence 2286, Ap
c 29	37	11.1	1934	7	US-11-293-697-2223	Sequence 2223, Ap
30	36.4	11.0	657	7	US-11-217-529-80796	Sequence 80796, A
31	36.4	11.0	1259	6	US-10-953-349-33671	Sequence 33671, A
32	36.4	11.0	2895	7	US-11-217-529-1899	Sequence 1899, Ap
33	36.4	11.0	3678	7	US-11-217-529-309	Sequence 309, App
34	36.2	10.9	600	7	US-11-217-529-77634	Sequence 77634, A
35	36.2	10.9	648	7	US-11-217-529-4648	Sequence 4648, Ap
36	36.2	10.9	840	7	US-11-217-529-933	Sequence 933, App
37	36.2	10.9	960	6	US-10-953-349-4197	Sequence 4197, Ap
c 38	36.2	10.9	2610	7	US-11-217-529-81636	Sequence 81636, A
39	36	10.8	1020	7	US-11-217-529-76749	Sequence 76749, A
40	36	10.8	1437	7	US-11-217-529-3524	Sequence 3524, Ap
41	36	10.8	1553	6	US-10-953-349-10321	Sequence 10321, A
42	36	10.8	1554	6	US-10-953-349-11554	Sequence 11554, A
43	36	10.8	1600	6	US-10-953-349-18505	Sequence 18505, A
44	36	10.8	2124	7	US-11-217-529-78847	Sequence 78847, A
45	36	10.8	2442	6	US-10-953-349-35802	Sequence 35802, A

ALIGNMENTS

RESULT 1

US-11-217-529-2794

; Sequence 2794, Application US/11217529

; Publication No. US20060099612A1

; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED

; APPLICANT: NAKAO, YOSHIHIRO

; APPLICANT: NAKAMURA, NORIHISA

; APPLICANT: KODAMA, YUKIKO

SCORE Search Results Details for Application 10626891 and Search Result us-10-626-891-1_copy_1_332.rst.

[Score Home](#)
[Page](#)

Retrieve Application List

SCORE System Overview

SCORE FAQ

Comments /
Suggestions

This page gives you Search Results detail for the Application 10626891 and Search Result us-10-626-891-1_copy_1_332.rst.

start

[Go Back to previous page](#)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 1, 2006, 13:19:39 ; Search time 3877.82 Seconds
(without alignments)
4787.540 Million cell updates/sec

Title: US-10-626-891-1_COPY_1_332
Perfect score: 332
Sequence: 1 ccagaaggtattatccaag.....atgtaagggcggaagtaac 332

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*
```

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	62	18.7	537	11	AZ702081	AZ702081 RPCI-23-2
2	62	18.7	540	11	AZ032908	AZ032908 RPCI-23-3
c 3	61.8	18.6	997	14	CNS005TE	AL060767 Drosophil
4	59.6	18.0	625	12	CE633607	CE633607 tigr-gss-
c 5	59.6	18.0	683	12	CE830234	CE830234 tigr-gss-
6	58.2	17.5	416	11	AZ652793	AZ652793 1M0526J10
c 7	58	17.5	336	11	AZ635799	AZ635799 1M0493L08
c 8	58	17.5	432	12	CE704975	CE704975 tigr-gss-
c 9	58	17.5	981	1	AL564376	AL564376 AL564376
c 10	57.2	17.2	473	11	AZ891439	AZ891439 RPCI-24-1
c 11	57.2	17.2	907	14	CNS021J4	AL176953 Tetraodon
c 12	56.2	16.9	440	11	AZ408774	AZ408774 1M0180D24
13	56.2	16.9	681	12	CE197701	CE197701 tigr-gss-
c 14	56.2	16.9	877	14	CR253706	CR253706 Forward s
c 15	56	16.9	486	12	CE764895	CE764895 tigr-gss-
16	56	16.9	666	4	BY751847	BY751847 BY751847
17	56	16.9	1376	10	DV780621	DV780621 Hw_Fat_35
18	56	16.9	3816	6	AK156998	AK156998 Mus muscu
19	55.8	16.8	578	14	DX361495	DX361495 MUGQ_CH25
20	55.8	16.8	639	14	CNS017QD	AL108367 Drosophil
c 21	55.4	16.7	769	14	AG464079	AG464079 Mus muscu
22	55.4	16.7	2525	6	AK159063	AK159063 Mus muscu
23	55.4	16.7	5215	6	AK157338	AK157338 Mus muscu
24	55.2	16.6	761	14	AG405712	AG405712 Mus muscu
c 25	55.2	16.6	1187	14	AG387118	AG387118 Mus muscu
26	55	16.6	298	12	CE521047	CE521047 tigr-gss-
27	55	16.6	625	11	AZ912416	AZ912416 RPCI-24-1
28	55	16.6	667	11	AZ600028	AZ600028 1M0416J09
29	55	16.6	675	12	CE006669	CE006669 tigr-gss-
c 30	55	16.6	698	7	AV728560	AV728560 AV728560
31	55	16.6	3276	6	AY325247	AY325247 Rattus no
32	54.8	16.5	519	11	BH062219	BH062219 RPCI-24-3
c 33	54.8	16.5	691	11	BH040136	BH040136 RPCI-24-2
34	54.8	16.5	733	11	AZ820077	AZ820077 2M0092M04
35	54.8	16.5	776	11	BH044827	BH044827 RPCI-24-2
c 36	54.8	16.5	781	14	AG565560	AG565560 Mus muscu
37	54.6	16.4	551	12	CE136192	CE136192 tigr-gss-
c 38	54.6	16.4	614	12	CE524492	CE524492 tigr-gss-
39	54.6	16.4	694	11	AZ948928	AZ948928 2M0212I12
40	54.6	16.4	712	12	CE419579	CE419579 tigr-gss-
c 41	54.6	16.4	750	14	AG496094	AG496094 Mus muscu
42	54.6	16.4	959	3	BU504923	BU504923 AGENCOURT
43	54.4	16.4	606	12	CE451752	CE451752 tigr-gss-
c 44	54.4	16.4	789	14	AG543016	AG543016 Mus muscu
45	54.2	16.3	448	2	BM540309	BM540309 hb20e10.g

ALIGNMENTS

RESULT 1

AZ702081

LOCUS AZ702081 537 bp DNA linear GSS 24-JAN-2001